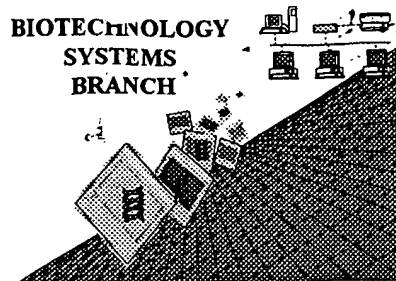


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/911,261

Source: OIRF

Date Processed by STIC: 8/1/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/911,261

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      Misaligned Amino  
    Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ✓ Variable Length  
Sequence(s) 1-2 contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      PatentIn 2.0  
    "bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)             . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      Skipped Sequences  
    (OLD RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8      Skipped Sequences  
    (NEW RULES)  
Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9      Use of n's or Xaa's  
    (NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ✓ Invalid <213>  
    Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11      Use of <220>  
Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown.". Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      PatentIn 2.0  
    "bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/911,261

DATE: 08/01/2001

TIME: 15:07:46

Input Set : A:\109845-130.txt

Output Set: N:\CRF3\08012001\I911261.raw

Does Not Comply  
Corrected Diskette Needed

pp 1,3,6-8

2 <110> APPLICANT: Sera, Takashi  
 4 <120> TITLE OF INVENTION: Zinc Finger Domain Recognition Code and Uses Thereof  
 6 <130> FILE REFERENCE: 109846-130  
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/911,261  
 C--> 8 <141> CURRENT FILING DATE: 2001-07-23  
 8 <150> PRIOR APPLICATION NUMBER: US 60/220,060  
 10 <151> PRIOR FILING DATE: 2000-07-21  
 12 <160> NUMBER OF SEQ ID NOS: 69  
 14 <170> SOFTWARE: PatentIn version 3.0

## ERRORED SEQUENCES

16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 28  
 18 <212> TYPE: PRT  
 19 <213> ORGANISM: Artificial Sequence  
 21 <220> FEATURE:  
 22 <223> OTHER INFORMATION: Zinc finger domain.  
 24 <220> FEATURE:  
 25 <221> NAME/KEY: VARIANT  
 26 <222> LOCATION: (1)..(28)  
 27 <223> OTHER INFORMATION: Amino acids 1-3, 8-19 and 25-28 are Xaa wherein Xaa = any  
 amino  
 28 acid.  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: VARIANT  
 32 <222> LOCATION: (5)..(6)  
 33 <223> OTHER INFORMATION: Amino acid 5 is Xaa wherein Xaa = any amino acid, amino acids  
 34 and 6 together represent from 2 to 4 amino acids in length.  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: VARIANT  
 38 <222> LOCATION: (21)..(23)  
 39 <223> OTHER INFORMATION: Amino acid 21 is Xaa wherein Xaa = any amino acid, amino  
 acids  
 40 21-23 together represent from 3 to 5 amino acids in length.  
 E--> 42 <400> SEQUENCE: 0  
 W--> 44 Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 45 1 10 15  
 W--> 47 Xaa Xaa Xaa His Xaa Xaa Xaa His Xaa Xaa Xaa Xaa  
 48 20 25  
 51 <210> SEQ ID NO: 2  
 52 <211> LENGTH: 28  
 53 <212> TYPE: PRT  
 54 <213> ORGANISM: Artificial Sequence  
 56 <220> FEATURE:  
 57 <223> OTHER INFORMATION: Zinc finger domain.

Xaa can only  
represent a single  
amino acid - variablelength  
not  
permitted  
see item 5  
on Enr  
summary  
sheet

59 <220> FEATURE:

60 <221> NAME/KEY: VARIANT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/911,261

DATE: 08/01/2001

TIME: 15:07:46

Input Set : A:\109845-130.txt

Output Set: N:\CRF3\08012001\I911261.raw

61 <222> LOCATION: (1)..(28)

63 <223> OTHER INFORMATION: Amino acids 1-3, 8-12, 14, 17-18 and 25-28 are Xaa wherein

Xaa =

64 any amino acid.

66 <220> FEATURE:

67 <221> NAME/KEY: VARIANT

68 <222> LOCATION: (5)..(6)

69 <223> OTHER INFORMATION: Amino acid 5 is Xaa wherein Xaa = any amino acid, amino acids

5 70 and 6 together represent from 2 to 4 amino acids in length. *item 5 on Enr sheet*

72 <220> FEATURE:

73 <221> NAME/KEY: VARIANT

74 <222> LOCATION: (21)..(23)

75 <223> OTHER INFORMATION: Amino acid 21 is Xaa wherein Xaa = any amino acid, amino

acids

76 21-23 together represent from 3 to 5 amino acids in length. *item 5*

78 <220> FEATURE:

79 <221> NAME/KEY: VARIANT

80 <222> LOCATION: (13)..(13)

81 <223> OTHER INFORMATION: Amino acid 13 is Xaa wherein Xaa = Z-1 wherein Z-1 = Arg or

Lys,

82 Gln or Asn, Thr, Met, Leu or Ile, or Glu or Asp.

84 <220> FEATURE:

85 <221> NAME/KEY: VARIANT

86 <222> LOCATION: (15)..(15)

87 <223> OTHER INFORMATION: Amino acid 15 is Xaa wherein Xaa = Z2 wherein Z2 = Ser or

Arg,

88 Asn Gln, Thr, Val or Ala, or Asp or Glu.

90 <220> FEATURE:

91 <221> NAME/KEY: VARIANT

92 <222> LOCATION: (16)..(16)

93 <223> OTHER INFORMATION: Amino acid 16 is Xaa wherein Xaa = Z3 wherein Z3 = His or

Lys,

94 Asn or Gln, Ser, Ala, or Val, or Asp or Glu.

96 <220> FEATURE:

97 <221> NAME/KEY: VARIANT

98 <222> LOCATION: (19)..(19)

99 <223> OTHER INFORMATION: Amino acid 19 is Xaa wherein Xaa = Z6 wherein Z6 = Arg or

Lys,

100 Gln or Asn, Thr, Tyr, Leu, Ile or Met, or Glu or Asp.

E--> 102 <400> SEQUENCE: 0 *p.6*

W--> 104 Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

105 1 5 10 15

W--> 107 Xaa Xaa Xaa His Xaa Xaa Xaa His Xaa Xaa Xaa Xaa

108 20 25

111 <210> SEQ ID NO: 3

112 <211> LENGTH: 196

113 <212> TYPE: PRT

114 <213> ORGANISM: Artificial Sequence

116 <220> FEATURE:

117 <223> OTHER INFORMATION: Zinc finger protein.

E--> 119 <400> SEQUENCE: 0 *p.6*

121 Val Pro Ile Pro Gly Lys Lys Lys Gln His Ile Cys His Ile Gln Gly

122	1				5					10					15	
124	Cys	Gly	Lys	Val	Tyr	Gly	Gln	Ser	Ser	Asp	Leu	Gln	Arg	His	Leu	Arg
125				20					25					30		

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/911,261

DATE: 08/01/2001

TIME: 15:07:46

Input Set : A:\109845-130.txt

Output Set: N:\CRF3\08012001\I911261.raw

```

127 Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys Gly
128      35      40      45
130 Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr His
131      50      55      60
133 Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe Met
134 65      70      75      80
136 Arg Ser Asp Glu Leu Ser Arg His Ile Lys Thr His Gln Asn Lys Lys
137      85      90      95
139 Asp Gly Gly Gly Ser Gly Lys Lys Lys Gln His Ile Cys His Ile Gln
140      100      105      110
142 Gly Cys Gly Lys Val Tyr Gly Thr Thr Ser Asn Leu Arg Arg His Leu
143      115      120      125
145 Arg Trp His Thr Gly Glu Arg Pro Phe Met Cys Thr Trp Ser Tyr Cys
146      130      135      140
148 Gly Lys Arg Phe Thr Arg Ser Ser Asn Leu Gln Arg His Lys Arg Thr
149 145      150      155      160
151 His Thr Gly Glu Lys Lys Phe Ala Cys Pro Glu Cys Pro Lys Arg Phe
152      165      170      175
154 Met Arg Ser Asp His Leu Ser Arg His Ile Lys Thr His Gln Asn Lys
155      180      185      190
157 Lys Gly Gly Ser
158      195

```

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6

delete extra bracket

<400> 1

same error as Seq. 2, Seq 3

Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

FBI

Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.



09/9/11, 261 2

<211> 45

<212> DNA

<213> Artificial Sequence (PCR Primer)

<2207

<2237

<400>

54

ttcagggcgg tctctcggt tctcgccagt gtgagtacgc tgatg

45

This goes on <2237 line, not <2137 line'

(see  
item 10  
on Euro  
summary  
sheet)

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8

<400> 69

Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Xaa Ser Xaa Xaa  
1 5 10 15

Leu Ser Xaa His Gln Arg Thr His Thr Gly Glu Lys  
20 25

109845-130.ST25

Page 1

*Delete*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/911,261

DATE: 08/01/2001

TIME: 15:07:47

Input Set : A:\109845-130.txt

Output Set: N:\CRF3\08012001\I911261.raw

L:8 M:270 C: Current Application Number differs, Replaced Current Application No  
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:42 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:1 differs:0  
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0  
L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0  
L:102 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:0  
L:104 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0  
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:0  
L:119 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:0  
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:562 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30  
L:835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31  
L:852 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32  
L:870 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33  
L:887 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34  
L:904 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:922 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36  
L:939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37  
L:956 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38  
L:973 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39  
L:991 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41  
L:1151 M:258 W: Mandatory Feature missing, <220> FEATURE:  
L:1151 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:  
L:1348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68  
L:1351 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68  
L:1389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69  
L:1392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69